

HG52.apr

		Section 1				
		(1)	1	10	20	30
AAH18130_PAR1L	(1)	----	MR	SP	SA	AWLLGAA
NP_001983_PAR1	(1)	----	MG	PR	RL	LLVAAC
NP_835230_P2Y8	(1)	----	-----	-----	-----	-----
TransBD243560_HG52	(1)	----	-----	-----	-----	-----
NP_004092_PAR3	(1)	-----	----	----	----	----
NP_005287_P2Y9	(1)	-----	----	----	----	----
P79928_XP2Y	(1)	-----	----	----	----	----
Consensus	(1)	-----	----	----	----	----
		Section 2				
		(46)	46	60	70	80
AAH18130_PAR1L	(41)	-----	----	----	----	----
NP_001983_PAR1	(46)	----	RNP	ND	KY	EPF
NP_835230_P2Y8	(1)	-----	-----	-----	-----	-----
TransBD243560_HG52	(1)	-----	-----	-----	-----	-----
NP_004092_PAR3	(39)	----	TFR	GAP	PNS	FEE
NP_005287_P2Y9	(1)	-----	-----	-----	-----	-----
P79928_XP2Y	(1)	-----	-----	-----	-----	-----
Consensus	(46)	-----	-----	-----	-----	-----
		Section 3				
		(91)	91	100	110	120
AAH18130_PAR1L	(64)	----	FS	AS	VL	TG
NP_001983_PAR1	(91)	----	DAS	GY	LT	SS
NP_835230_P2Y8	(12)	----	AT	LO	ML	RN
TransBD243560_HG52	(12)	----	AT	LO	ML	RN
NP_004092_PAR3	(83)	----	AT	MG	YLT	SS
NP_005287_P2Y9	(28)	----	NN	TC	IV	DD
P79928_XP2Y	(32)	----	ED	TC	IV	DD
Consensus	(91)	----	TL	ML	V	LP
		Section 4				
		(136)	136	150	160	170
AAH18130_PAR1L	(109)	----	PA	VT	YMAN	LAL
NP_001983_PAR1	(136)	----	PA	VV	YML	HL
NP_835230_P2Y8	(57)	----	PS	VI	FMIN	LS
TransBD243560_HG52	(57)	----	PS	VI	FMIN	LS
NP_004092_PAR3	(127)	----	CT	TV	YTN	LAT
NP_005287_P2Y9	(73)	----	ET	AT	FT	IN
P79928_XP2Y	(77)	----	PT	TV	YMF	NL
Consensus	(136)	----	PT	VI	FMIN	LS

Section 5

	(181)	181	190	200	210	225
AAH18130_PAR1L (154)		FFYGNMYCSIL	FMTCISV	QRYWVI	NP	MGHSRKK-ANIAIGISLA
NP_001983_PAR1 (181)		AFYCNMYASILL	MTVISID	RFLAVV	PMQSL	SWRTLGRASFTCLA
NP_835230_P2Y8 (102)		AFYANMYSSILT	MTCISV	ERFLGV	LYPLSS	KRWRRRRYAVAACAG
TransBD243560_HG52 (102)		AFYANMYSSILT	MTCISV	ERFLGV	LYPLSS	KRWRRRRYAVAACAG
NP_004092_PAR3 (172)		IFYGNMYCSILL	LACISIN	RYLAIV	HPFTY	RGLPKHTYALVTCGL
NP_005287_P2Y9 (117)		AFLTNIYGSML	FLTCISV	DRFLAIV	YPFRS	RTITRNSAIVCAG
P79928_XP2Y (122)		LFYANLYSSIL	FLTCISV	HRYRGV	CHPITS	LRMNAKHAYVICAL
Consensus (181)		AFYANMYSSIL	MTCISV	DRFLAVV	YPLSSK	R RYAV CAG

Section 6

	(226)	226	240	250	260	270
AAH18130_PAR1L (198)		TWLLTLLVTI	PYVVKQ	TIFIPAT	NITTC	HDVLEPEQLL--VGDMF
NP_001983_PAR1 (226)		EWALAIAGV	VPVLKE	QTIQVPG	LNITTC	HDVLENETLL--EGYYA
NP_835230_P2Y8 (147)		TWLLLLTALS	PLARTD	LTPVHAL	GIITC	FDVLKWTMLPSVAMWA
TransBD243560_HG52 (147)		TWLLLLTALS	PLARTD	LTPVHAL	GIITC	FDVLKWTMLPSVAMWA
NP_004092_PAR3 (217)		VWATVFLY	MLFFIL	KQEYYL	VQPDIT	TCHDVHNTCES--SSPFQL
NP_005287_P2Y9 (162)		VWILVLSG	GISASL	FSTNVN	NAT--T	TCFEGFSKRW--KTYLS
P79928_XP2Y (167)		VWLSVTLC	LVENLI	IFVTVS	PKVKN--	TICHDTRPEDF--ARYV
Consensus (226)		VWLLVL	ALIPL I	T V AL	ITTCHD	VL LL A WA

Section 7

	(271)	271	280	290	300	315
AAH18130_PAR1L (241)		NYFLSLAIG	VFTFPA	FLTASAY	VLMIRM	LRSAMDENS---EKKR
NP_001983_PAR1 (269)		YFSAFSAV	FFVPLT	IISTVC	YVSIIR	CLSSAVANRS---KKS
NP_835230_P2Y8 (192)		VFLFTTFIL	LLFPI	PFVITV	ACYTAT	ILKLLRTEEAHGR---EQRR
TransBD243560_HG52 (192)		VFLFTTFIL	LLFPI	PFVITV	ACYTAT	ILKLLRTEEAHGR---EQRR
NP_004092_PAR3 (261)		YFISLAFF	GFLIP	FMLITY	CYAAIT	RTLN---AYDHR---WLWY
NP_005287_P2Y9 (203)		KITIFIEV	VGFIIP	LILNV	SCSSV	VLRTLRLPATLSQI---GTNR
P79928_XP2Y (207)		EYSTAIMC	LLFGIT	PCLIIA	GCYGL	MTRLMKPIVSGNQOTLPSYK
Consensus (271)		Y SI	ILLFLIP	VITVAC	Y AIIR	L KS A R

Section 8

	(316)	316	330	340	350	360
AAH18130_PAR1L (283)		KRAIKLIV	SVLAMY	LTCTPS	NILLV	VHYFLIKSQGQ-----SHV
NP_001983_PAR1 (311)		--ALFLS	AAVFCIF	ILICFG	PTNVLE	IAHYSFLSHTST-----TEAA
NP_835230_P2Y8 (234)		--RAVGLA	AAVLLT	AEVTC	FAPNNF	VLLAHIVSRIFYG-----KSY
TransBD243560_HG52 (234)		--RAVGLA	AAVLLT	AEVTC	FAPNNF	VLLAHIVSRIFYG-----KSY
NP_004092_PAR3 (300)		---VKASL	LILVIF	TICFAP	SNILII	HHANYYYNN-----TDGL
NP_005287_P2Y9 (245)		KKVLKMIT	VHMAFV	VCVPY	NSVFLY	ALVRSQAITNCFLERF
P79928_XP2Y (252)		KRSIKTI	IFVMTA	FAICF	MPFHTI	TRTLYYARLLGIK-CYALNVI
Consensus (316)		RAVKLA	VLLIFVIC	FAP NIV	LILHY	R

Section 9

	(361)	361	370	380	390	405
AAH18130_PAR1L (323)		YALYI	VALCLSTLNS	CIDPFVYYFVSH	DERDHAKNAL	LCRSVR--
NP_001983_PAR1 (350)		YFAYLL	CVCVSSISS	CIDPLIYYFAS	SECORYVYSIL	CKESSD-
NP_835230_P2Y8 (272)		YHVKLT	TLCLSLNNCL	DPFVYFASRE	FQLRLREYLG	CRRVPR-
TransBD243560_HG52 (272)		YHVKLT	TLCLSLNNCL	DPFVYFASRE	FQLRLREYLG	CRRVPR-
NP_004092_PAR3 (337)		YFIYLI	ALCLGSLNS	CIDPFLYFLM	SKTRNHSTAY	LTK-----
NP_005287_P2Y9 (290)		KIMYPIT	LCLATLNC	CFDPFIYYF	TLESFQKSFY	INAHIRMESL-
P79928_XP2Y (296)		NVTYKV	TRPLASANS	CIDPILYEL	ANDRYRRRL	IIRTVRRSSVPN
Consensus (361)		Y VY	LTCLSSLNS	CIDPFVYYFAS	EFQ L	L CR

Section 10

	(406)	406	420	430	440	450
AAH18130_PAR1L (366)		----	TVKQMQVSLT	SKKHSRKS	SSYSSSSTTV	KTSY-----
NP_001983_PAR1 (394)		----	PSSYNSSGQL	MASKMDTC	SNLNNSIYK	LLT-----
NP_835230_P2Y8 (316)		----	DTLDTTRRES	SLFSARTTS	SVRSEAGAH	PEGMEGATRPGLQRQE
TransBD243560_HG52 (316)		----	DTLDTTRRES	SLFSARTTS	SVRSEAGAH	PEGMEGATRPGLQRQE
NP_004092_PAR3 (375)		----	----	----	----	----
NP_005287_P2Y9 (334)		----	FKTETPLT	TKPSLP	AIQEEVSDQT	TNNGELMLESTF----
P79928_XP2Y (341)		RRCMH	INHPQTEPHM	TAGPLPVI	SAEEIPSN	CSMVRDENGEGSRE
Consensus (406)			T	SL SAK	S	G

Section 11

	(451)	451	460	470	480	495
AAH18130_PAR1L (398)		-----	-----	-----	-----	-----
NP_001983_PAR1 (426)		-----	-----	-----	-----	-----
NP_835230_P2Y8 (357)		SVF-----	-----	-----	-----	-----
TransBD243560_HG52 (357)		SVF-----	-----	-----	-----	-----
NP_004092_PAR3 (375)		-----	-----	-----	-----	-----
NP_005287_P2Y9 (371)		-----	-----	-----	-----	-----
P79928_XP2Y (386)		HRVEWTD	TKEINQMMN	RRSTIKRN	STDKNDM	KENRHGENYLPYVE
Consensus (451)						

Section 12

	(496)	496	510	520	530	540
AAH18130_PAR1L (398)		-----	-----	-----	-----	-----
NP_001983_PAR1 (426)		-----	-----	-----	-----	-----
NP_835230_P2Y8 (360)		-----	-----	-----	-----	-----
TransBD243560_HG52 (360)		-----	-----	-----	-----	-----
NP_004092_PAR3 (375)		-----	-----	-----	-----	-----
NP_005287_P2Y9 (371)		-----	-----	-----	-----	-----
P79928_XP2Y (431)		VVEKEDY	ETKREN	KTTEQSS	KTNAEQDEL	QTQIDSRLKRGKWQL
Consensus (496)						

Section 13

	(541)	541	550	560	570	585
AAH18130_PAR1L (398)		-----	-----	-----	-----	-----
NP_001983_PAR1 (426)		-----	-----	-----	-----	-----
NP_835230_P2Y8 (360)		-----	-----	-----	-----	-----
TransBD243560_HG52 (360)		-----	-----	-----	-----	-----
NP_004092_PAR3 (375)		-----	-----	-----	-----	-----
NP_005287_P2Y9 (371)		-----	-----	-----	-----	-----
P79928_XP2Y (476)		SSKKGAAQ	ENEKGHMEPS	FEGEGTSTWN	LLTPKMYGKK	DRLAKNV
Consensus (541)						

Section 14

	(586)	586	602
AAH18130_PAR1L (398)		-----	-----
NP_001983_PAR1 (426)		-----	-----
NP_835230_P2Y8 (360)		-----	-----
TransBD243560_HG52 (360)		-----	-----
NP_004092_PAR3 (375)		-----	-----
NP_005287_P2Y9 (371)		-----	-----
P79928_XP2Y (521)		EEVGYGKE	KEKELQNFPA
Consensus (586)			